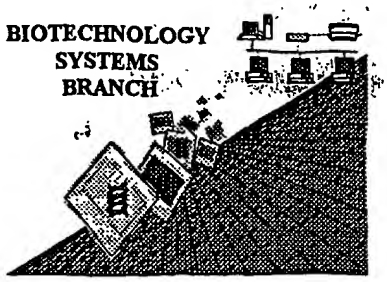
OIPE
SEP 07 2001
PATENT & TRADEMARK OFFICE

0420

# RAW SEQUENCE LISTING ERROR REPORT




**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 09/834,229

Source: OIPE

Date Processed by STIC: 4/30/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**
**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**
**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**
**http://www.uspto.gov/web/offices/pac/checker**

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# Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/834229

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

| | | |
|---|---|---|
| 1 ____ | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 ____ | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 J | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 ____ | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 ____ | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 √ | Variable Length | Sequence(s) 3 contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 ____ | PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.** |
| 8 ____ | Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:<br>**(2) INFORMATION FOR SEQ ID NO:X:**<br>**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br>**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**<br>**This sequence is intentionally skipped**<br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s) |
| 9 ____ | Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.<br>**<210> sequence id number**<br>**<400> sequence id number**<br>**000** |
| 10 ____ | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 J | Use of "Artificial" (NEW RULES) | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence. |
| 12 ____ | Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"<br>**Please explain source of genetic material in <220> to <223> section.**<br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 ____ | PatentIn ver. 2.0 "bug" | **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

AMC - Biotechnology Systems Branch - 4/06/2001

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/934,229

DATE: 04/30/2001
TIME: 11:03:16

pgs 1-3

Does Not Comply
Corrected Diskette Needed

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

```
  3 <110> APPLICANT: Efendic, Suad
  5 <120> TITLE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF MYOCARDIAL INFARCTION
  7 <130> FILE REFERENCE: X-10822A
OK> 9 <140> CURRENT APPLICATION NUMBER: US/09/834,229
  9 <141> CURRENT FILING DATE: 2001-04-12
  9 <150> PRIOR APPLICATION NUMBER: US 60/024,980
 10 <151> PRIOR FILING DATE: 1996-08-30
 12 <150> PRIOR APPLICATION NUMBER: US 08/915,918
 13 <151> PRIOR FILING DATE: 1997-08-21
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 31
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1
 26 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 27 1               5                  10                  15
 29 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 30             20                  25                  30
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 31
 34 <212> TYPE: PRT
C--> 35 <213> ORGANISM: Artificial  see item 11 on Error Summary Sheet
 37 <220> FEATURE:                  (see item 3 on Error Summary Sheet
 38 <223> OTHER INFORMATION: synthetic construct   (line exceeds 72 characters)
 40 <220> FEATURE:
 41 <221> NAME/KEY: VARIANT
 42 <222> LOCATION: (1)..(1)
 43 <223> OTHER INFORMATION. Xaa at position 1 is L-histidine, D-histidine, desamino-histidine
 44       , 2-amino-histidine, B-hydroxy-histidine, homohistidine, alpha-fl
 45       uoromethyl-histidine, and aplpha-methyl-histidine <-insert
 48 <220> FEATURE:                                                    Ala?
 49 <221> NAME/KEY: VARIANT
 50 <222> LOCATION: (2)..(2)
 51 <223> OTHER INFORMATION: Xaa at position 2 is Ala, Gly, Val, Thr, Ile, and alpha-methyl-Al
 55 <220> FEATURE:
 56 <221> NAME/KEY: VARIANT
 57 <222> LOCATION: (15)..(15)
 58 <223> OTHER INFORMATION: Xaa at position 15 is Glu, Gln, Ala, Thr, Ser, and Gly
 61 <220> FEATURE:
 62 <221> NAME/KEY: VARIANT
 63 <222> LOCATION: (21)..(21)
 64 <223> OTHER INFORMATION: Xaa at position 21 is Glu, Gln, Ala, Thr, Ser, and Gly
 67 <220> FEATURE:
 68 <221> NAME/KEY: VARIANT
 69 <222> LOCATION: (31)..(31)
```

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RAW SEQUENCE LISTING DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229 TIME: 11:03:17

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

70 <223> OTHER INFORMATION: Xaa at position 31 is NH2 and Gly-OH
73 <400> SEQUENCE: 2
W--> 75 Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly
76 1 5 10 15
W--> 78 Gln Ala Ala Lys Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
79 20 25 30
81 <210> SEQ ID NO: 3
82 <211> LENGTH: 28
83 <212> TYPE: PRT
C--> 84 <213> ORGANISM: Artificial
86 <220> FEATURE:
87 <223> OTHER INFORMATION: synthetic construct
89 <220> FEATURE:
90 <221> NAME/KEY: VARIANT
91 <222> LOCATION: (28)..(28)
92 <223> OTHER INFORMATION: Xaa at position 28 is Lys and Lys-Gly
95 <400> SEQUENCE: 3
97 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
98 1 5 10 15
W--> 100 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Xaa
101 20 25
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 30
105 <212> TYPE: PRT
C--> 106 <213> ORGANISM: Artificial
108 <220> FEATURE:
109 <223> OTHER INFORMATION: synthetic construct
111 <220> FEATURE:
112 <221> NAME/KEY: VARIANT
113 <222> LOCATION: (19)..(19)
114 <223> OTHER INFORMATION: Xaa at position 19 is Lys or Arg
117 <220> FEATURE:
118 <221> NAME/KEY: VARIANT
119 <222> LOCATION: (30)..(30)
120 <223> OTHER INFORMATION: Xaa at position 30 is Gly-OH or NH2
123 <400> SEQUENCE: 4
125 Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln
126 1 5 10 15
W--> 128 Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
129 20 25 30
131 <210> SEQ ID NO: 5
132 <211> LENGTH: 30
133 <212> TYPE: PRT
C--> 134 <213> ORGANISM: Artificial
136 <220> FEATURE:
137 <223> OTHER INFORMATION: synthetic construct
139 <400> SEQUENCE: 5
141 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
142 1 5 10 15

Xaa can only represent a single amino acid, nothing else

see item 11

Xaa can only represent a single amino acid. Variable length is not acceptable — see item 6 on Error Summary Sheet

item 11

invalid use of Xaa

item 11

item 11

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RAW SEQUENCE LISTING DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229 TIME: 11:03:17

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

```
144 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
145             20                  25                  30
147 <210> SEQ ID NO: 6
148 <211> LENGTH: 4
149 <212> TYPE: PRT
C--> 150 <213> ORGANISM: Artificial
152 <220> FEATURE:
153 <223> OTHER INFORMATION: synthetic construct
155 <400> SEQUENCE: 6
157 Ser Arg Arg Gln
158 1
```

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VERIFICATION SUMMARY DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229 TIME: 11:03:18

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:84 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:134 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:150 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6